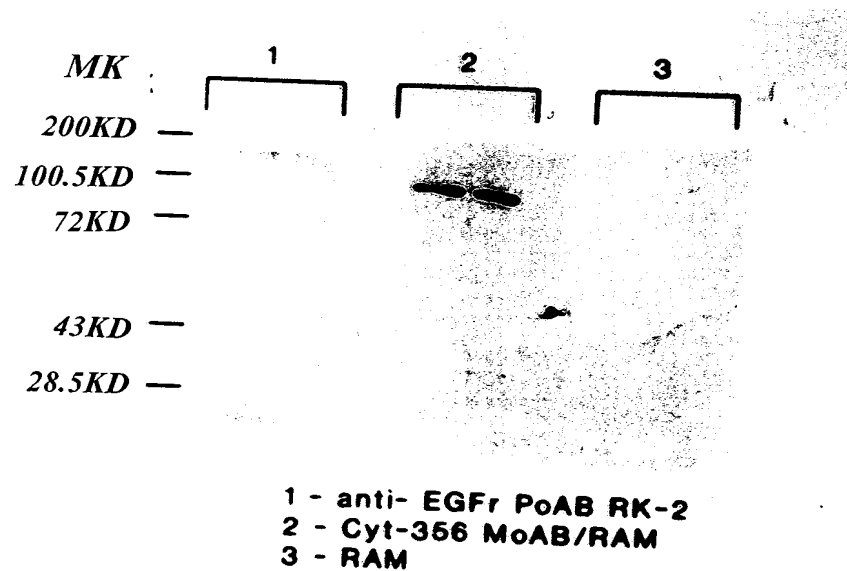




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FIGURE 1



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BEST AVAILABLE COPY

FIGURE 2B



FIGURE 2A



FIGURE 2D



FIGURE 2C



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FIGURE 3B



FIGURE 3D



FIGURE 3A

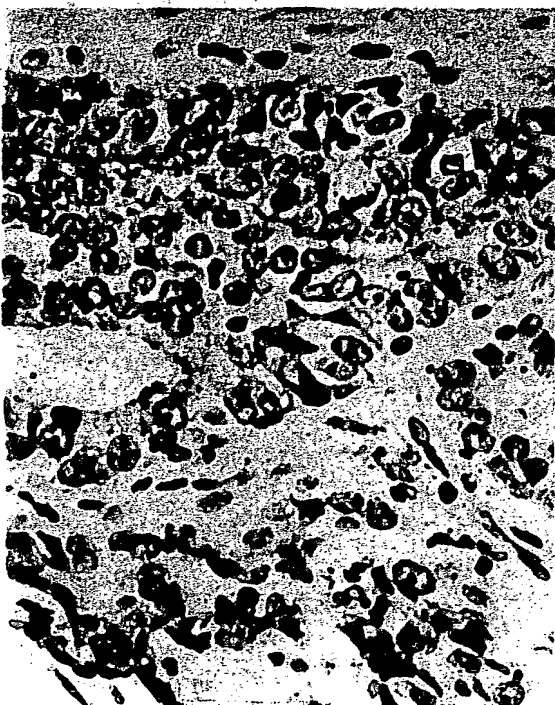
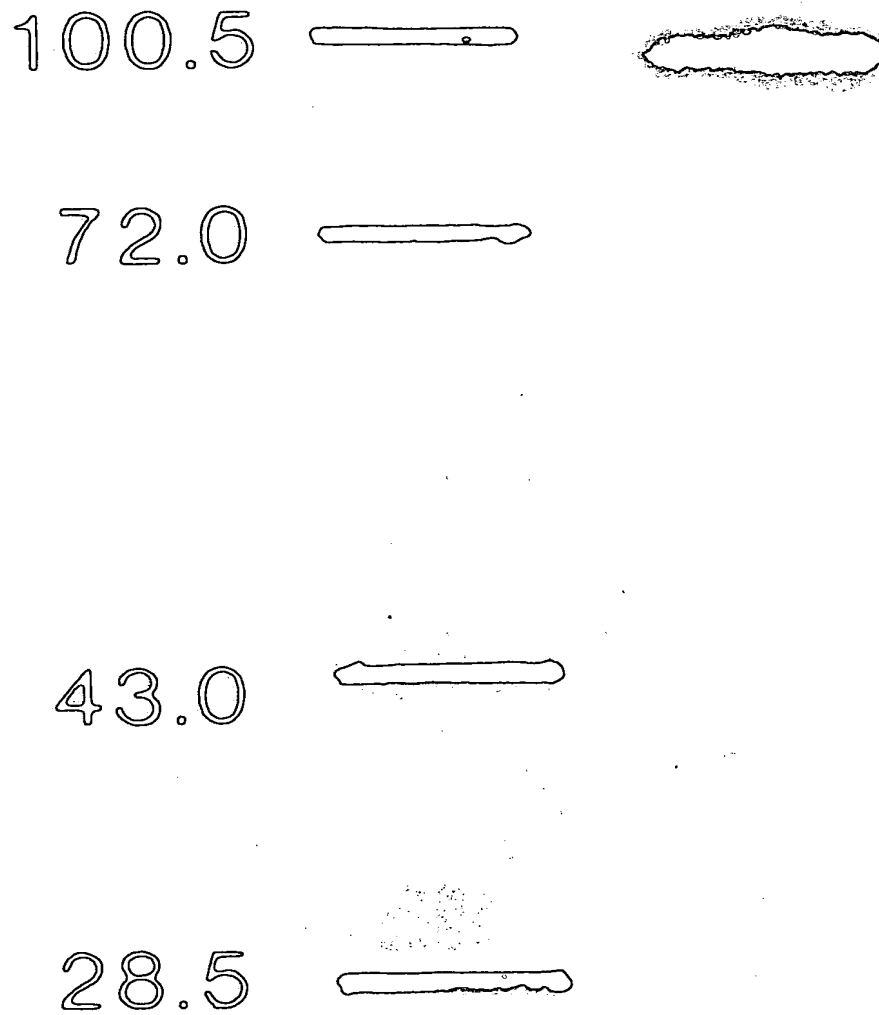


FIGURE 3C



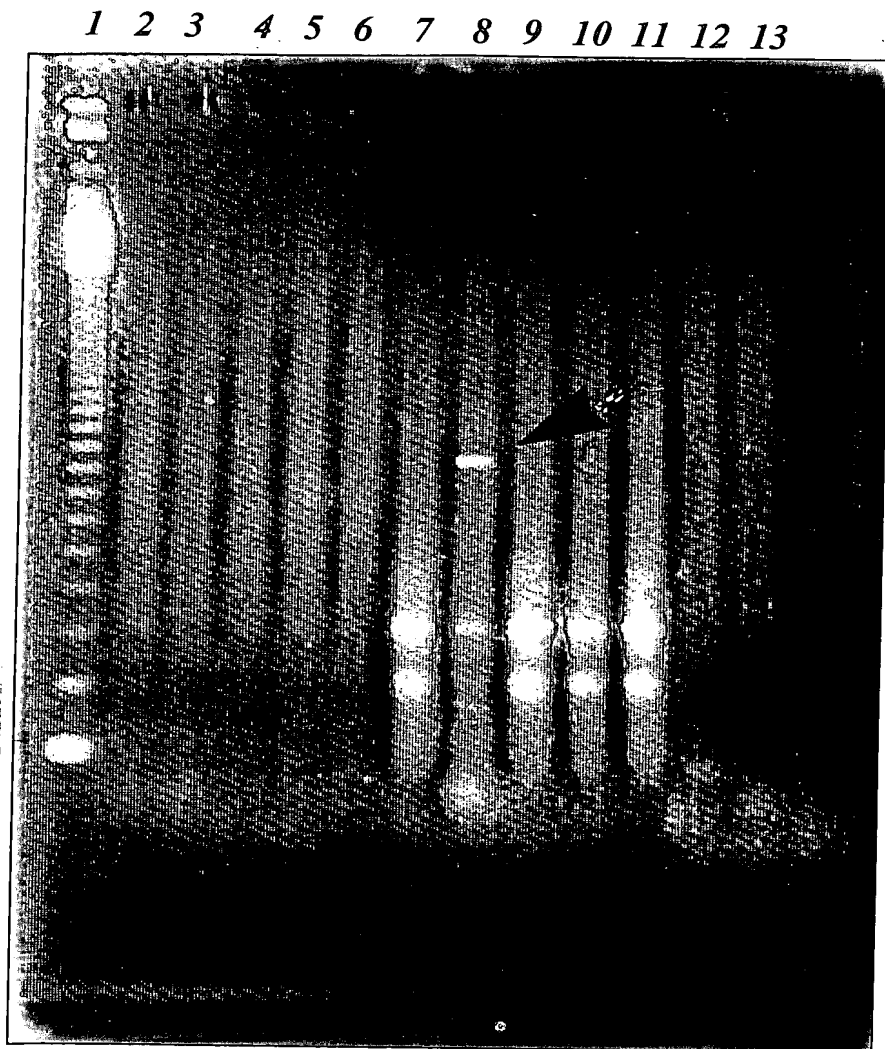
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FIGURE 4



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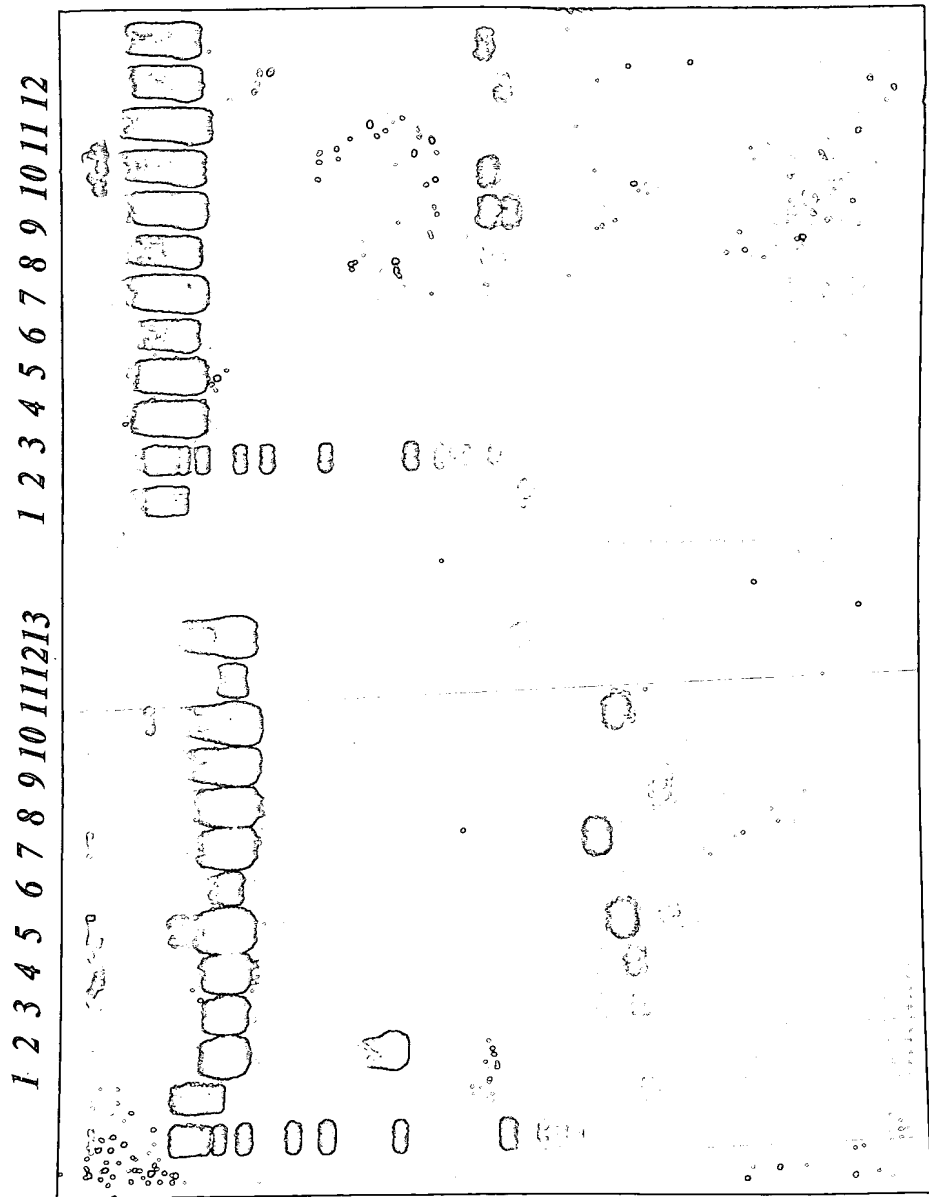
FIGURE 5



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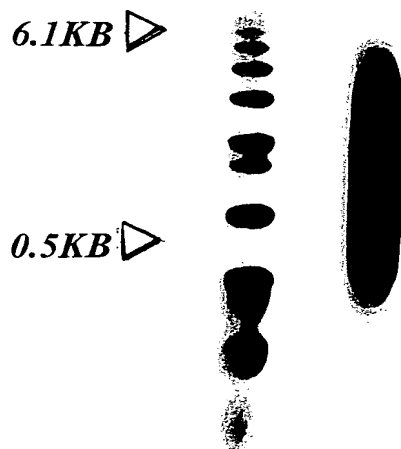
FIGURE 6A

FIGURE 6B



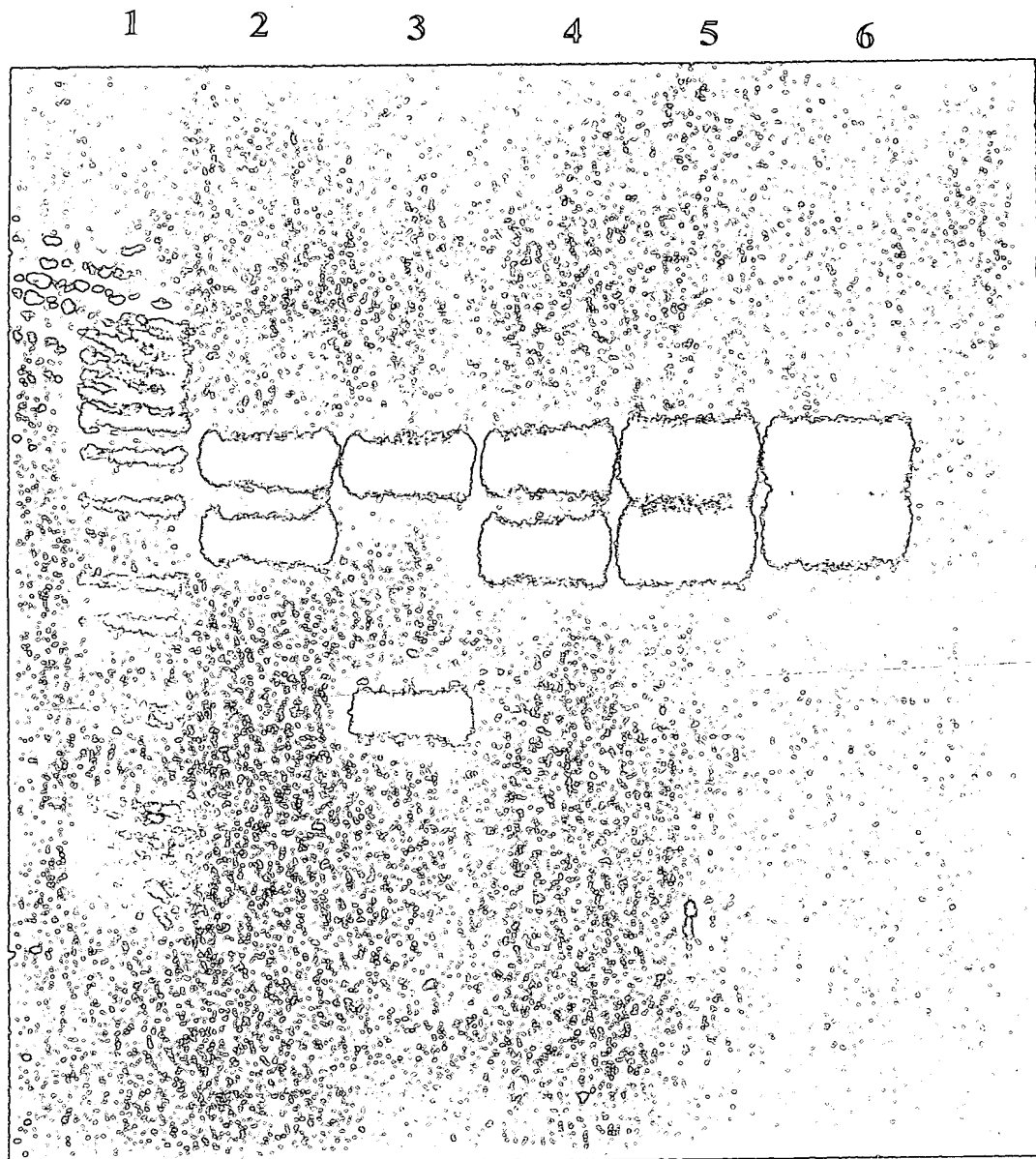
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FIGURE 7



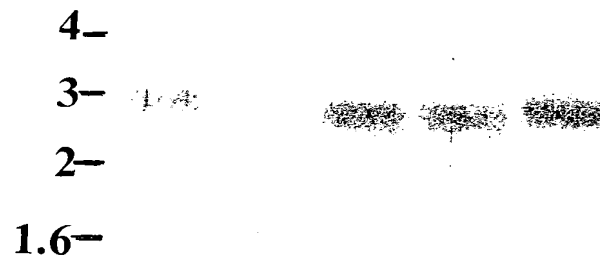
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FIGURE 8



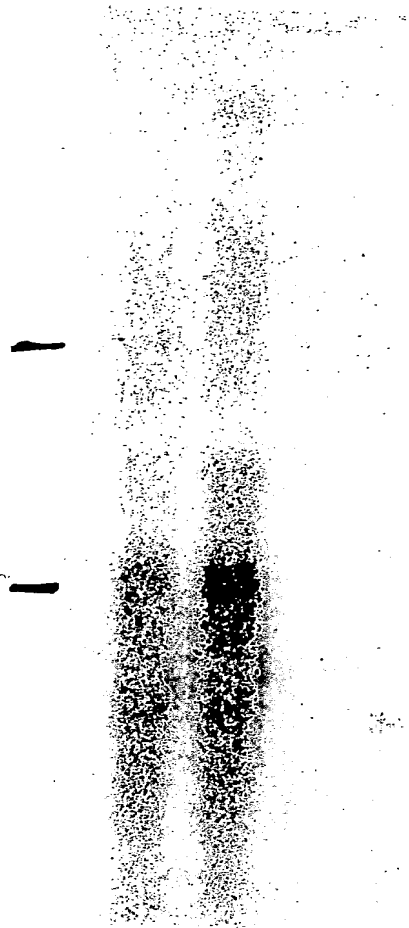
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FIGURE 9



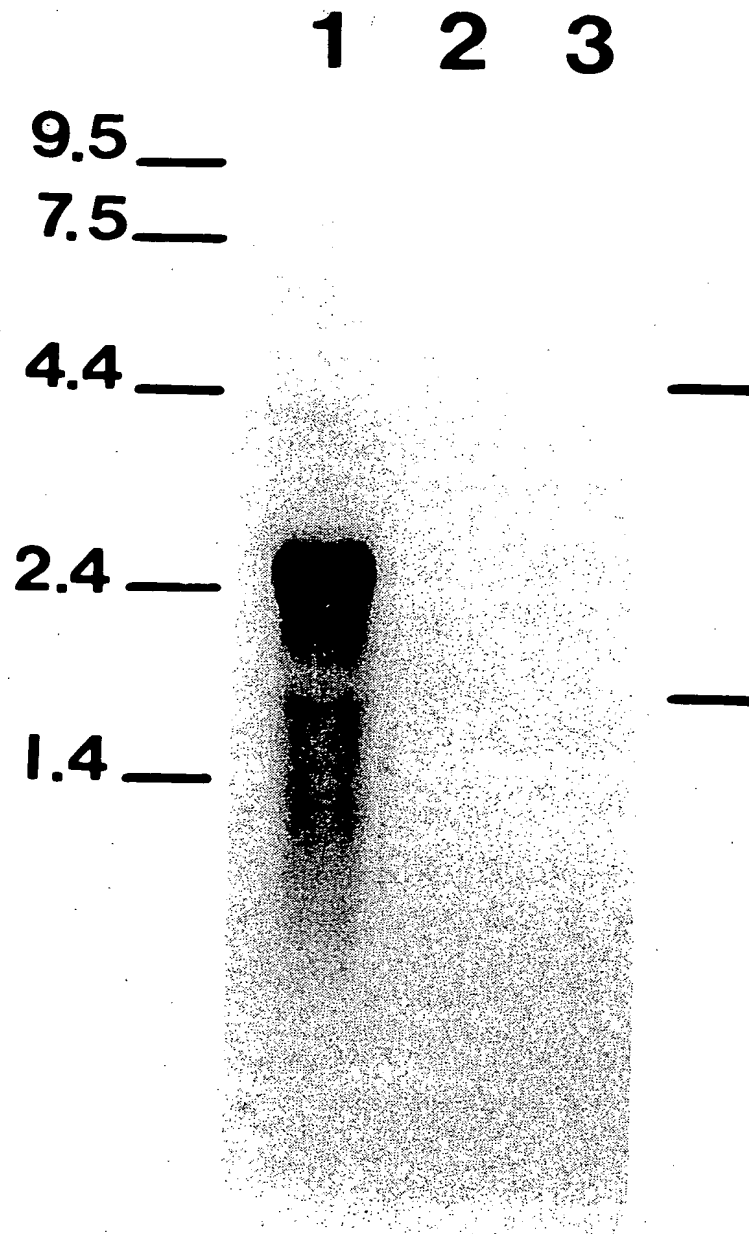
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FIGURE 10



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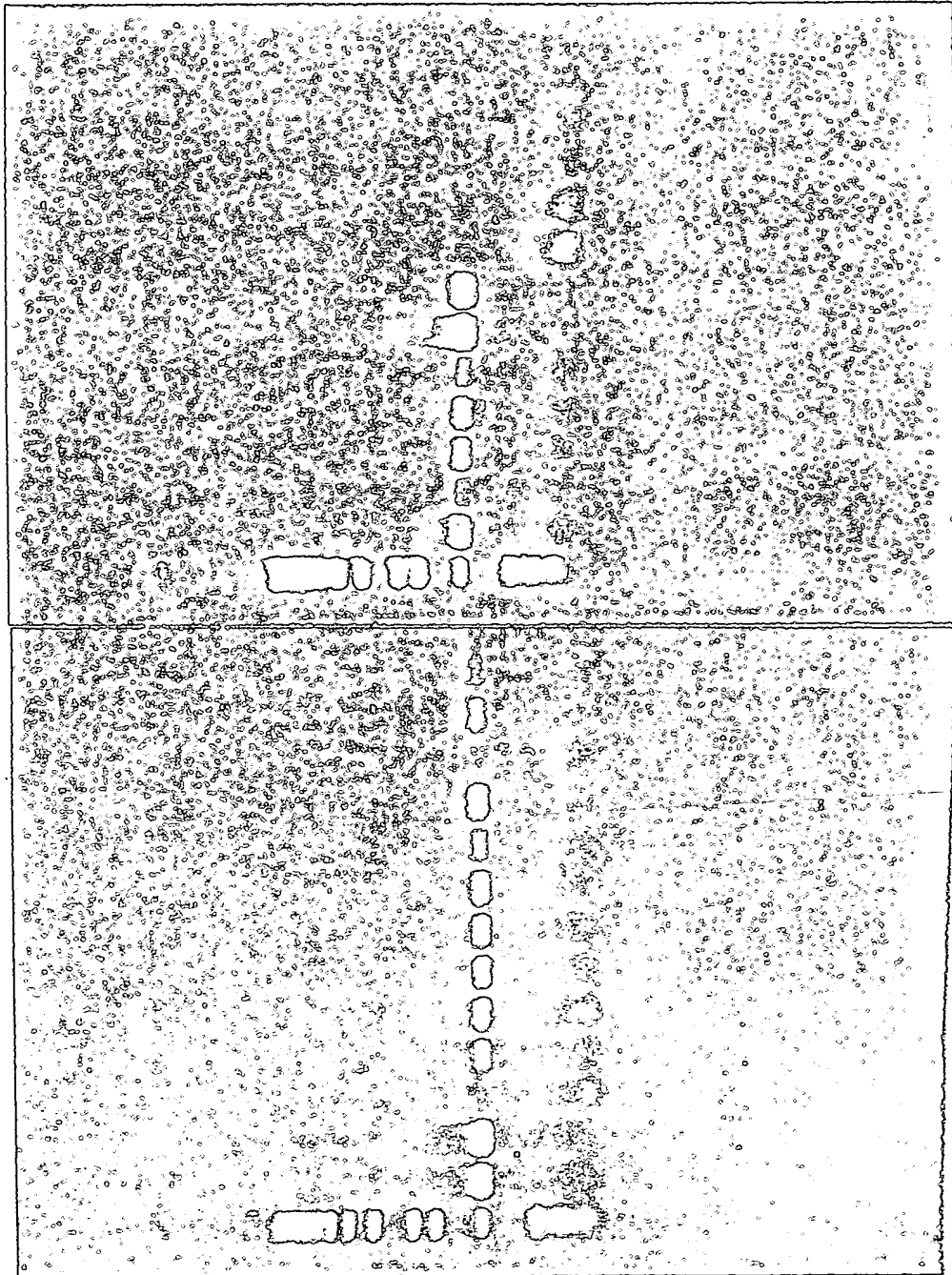
FIGURE 11



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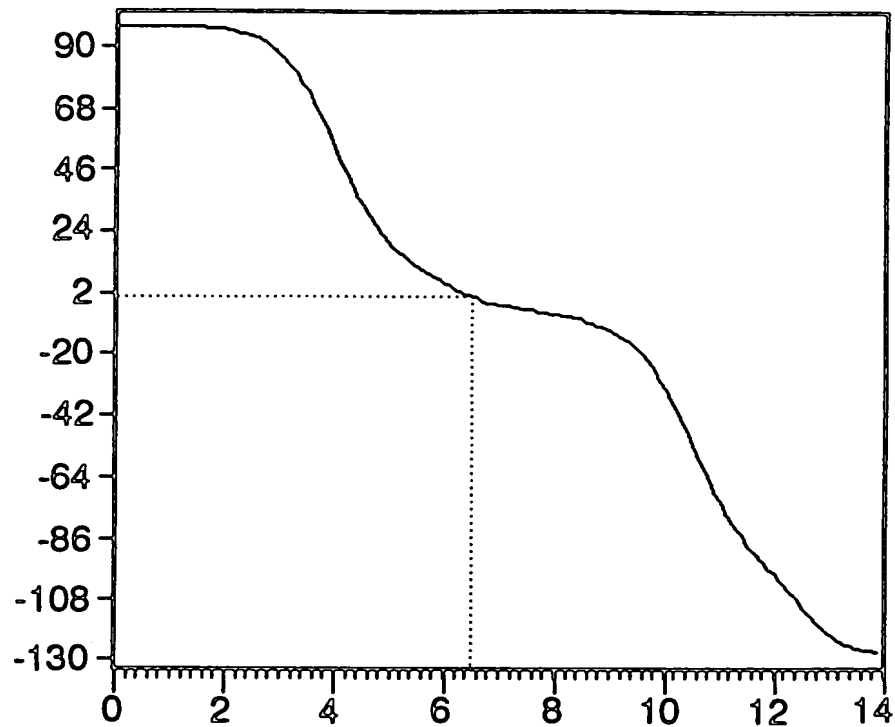
FIGURE 12B

0 1 2 3 4 5 6 7 8 9 10 11 12 13 0 14 15 16 17 18 19 20



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FIG. 13



Done on sequence PMSANTIGEN.
Total number of residues is: 750.
Analysis done on the complete sequence.

In Helical	(H)	conformation	[DC =	-75	CNAT]	:	264	AA =>	35.2%
In Extended	(E)	conformation	[DC =	-88	CNAT]	:	309	AA =>	41.2%
In Turn	(T)	conformation	[DC =	0	CNAT]	:	76	AA =>	10.1%
In Coil	(C)	conformation	[DC =	0	CNAT]	:	101	AA =>	13.4%

Sequence shown with conformation codes.

Consecutive stretch of 5 or more residues in a given conformation are overlined.

1	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H
31	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E	E
61	H	H	H	H	H	H	H	H	H	H	H	H	H	H	E	E	E	E	C	C	C	C	H

[illegible]

FIG. 14-3

451	E E C E T E E E E E E E E E E E E E E E E H
481	H C H H H H H H H H H H H H H H H H H H H
511	E E E E C C C C C C C C C C C C C C C C C T
541	T E T T T C E E E E E E E E E E E E E E H
571	H H
601	H E
631	H E
661	E E H H H H H H H H H H H H H H H H H H E
691	E E E T C C C H H H H H H H H H H H H H C
721	C H

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FIG. 14-4

Semi-graphical output.
=====

Symbols used in the semi-graphical representation:

Helical conformation: X	Extended conformation: -
Turn conformation: >	Coil conformation: *

10	20	30	40	50
MWNLHETDSAVATARRPRWLCAGALVLAGGFLLGFLFGWFIKSSNEAT				
XXXXXXXXXXXXX>>>-----XXXXXXXXXXXXX>>>X				
XXXXXXXXXXXXX>>>-----XXXXXXXXXXXXX>>>X				
60	70	80	90	100
NITPKHNMKAFDELKAENIKKFLYNFTQIPHLAGTEQNFQLAKQIQSQW				

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FIG. 14-5

```
XXXXXXXXXXXXXXXXXX-->>-->XXXXXXXXXX-X*-  
XXXXXXXXXXXXXXXXXX-->>-->XXXXXXXXXX-X*-  
  
110      120      130      140      150  
|         |         |         |  
KEFGDVELAHYDVLLSYPNKTHPNYISINEDGNEIFNTSLFEPPPG  
  
->>*>*>*>*>*>*>*>*>*>*>*>*>*>*>*>*>*>  
->>*>*>*>*>*>*>*>*>*>*>*>*>*>*>*>*>*>  
  
160      170      180      190      200  
|         |         |         |  
YENVSDIVPPFSAFSPQGMPEGLVYVNYARTEDFFKLERDMKINCSGKI
```

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FIG. 14-6

```
>----->*>*>-----XXXXXXXXXXXXXXXXXX>>--
>----->*>*>-----XXXXXXXXXXXXXXXXXX>>--
>----->*>*>-----XXXXXXXXXXXXXXXXXX>>--

210      220      230      240      250
|         |         |         |
VIARYGVFRGNKVNQAQLAGAKGVILYSDPADYFAPGVKSYPDGWNLPG

----->>*>*>*>----->>----->>*>
----->>*>*>*>----->>----->>*>

260      270      280      290      300
|         |         |         |
GGVQRGNILNLNGAGDPLTPGYPANEYAYRRGIAEAVGLPSIPVHPIGYY

>*>----->>*>*>*>-----XX-----
>*>----->>*>*>*>-----XX-----

310      320      330      340      350
|         |         |         |
DAQKLEKMGGSAPPDSSWRGSLKVPYNVGPFGFTGNFSTQKVKTHISTN

XXXXXXXXXX->>*>*>*>----->>----->>*>
XXXXXXXXXX->>*>*>*>----->>----->>*>

360      370      380      390      400
|         |         |         |
EVTRIYNVIGTLRGAVEPDRYVILGGHRDSWVFGIDPQSGAAVVHEIVR
```

```

-----XX
-----XX
410      420      430      440      450
|         |         |         |         |
SFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEWAEENSRLQLQERGVAI
|
XXXXXX>>>XX>-----XXXXXXXXXXXXXXXX-----
XXXXXX>>>XX>-----XXXXXXXXXXXXXXXX-----
460      470      480      490      500
|         |         |         |         |
NADSSIEGNYTLRVDCTPLMYSLVHNLTKEKSPDEGFEGKSLYESWTKK
|
-----XX>>-----XXXXXXXXXXXXXXXXXX>>>XX>
-----XX>>-----XXXXXXXXXXXXXXXXXX>>>XX>
510      520      530      540      550
|         |         |         |         |
SPSPFSGMPRIKLGSGNDFEVFFQRLGIASGRARYTKNWEKNKFSGYP
|
XX>-----XX>XX>XX>XX>XX>XX>XX>XX>XX>XX>XX>
XX>-----XX>XX>XX>XX>XX>XX>XX>XX>XX>XX>XX>
560      570      580      590      600
|         |         |         |         |

```

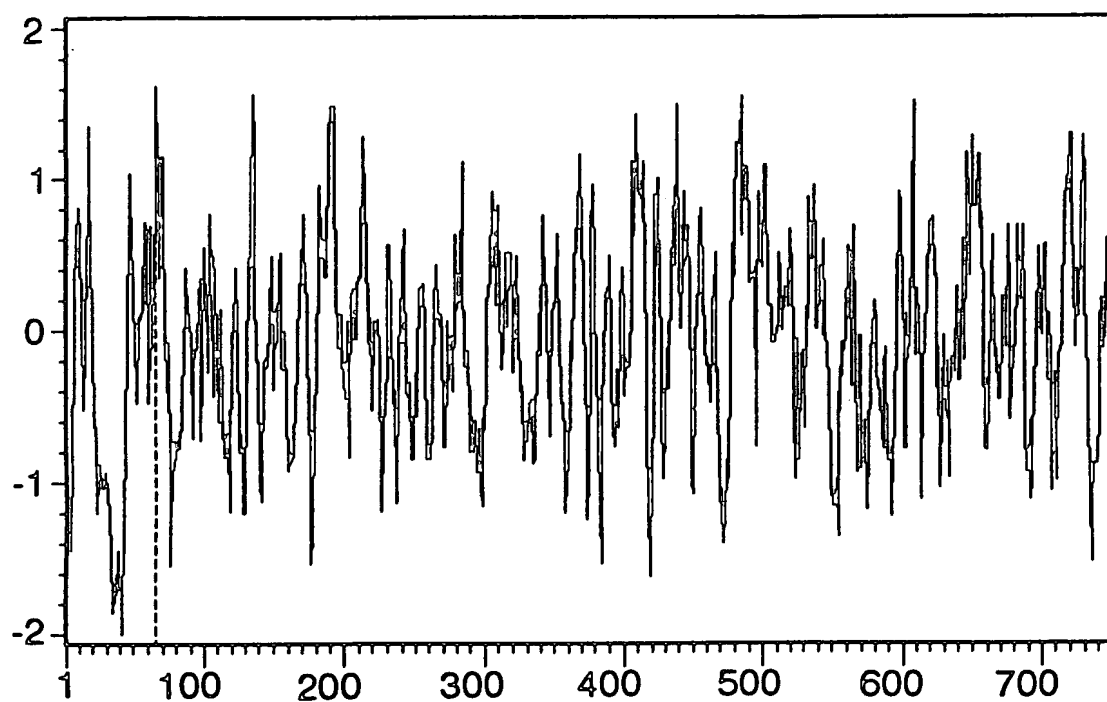
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FIG. 14-8

LYHSVETVELVEFYDPMFKYHLLTVAQVRGGMVFELANSIVLPFDCRDY
-----XXXXXXXXXXXXX-X-----XXXXXXXX----->XXX
-----XXXXXXXXXXXXXXX-X-----XXXXXXXX----->XXX
610 620 630 640 650
| | | | |
AVVLRKYADKIIYSISMKHPQEMKTYSVSFDLSLFSVKNFTETIASKFSERL
XXXXXXXXXX-----X*XXXXXXXX-----XXXXXXXXXXXXXXXXXXXX
XXXXXXXXXX-----X*XXXXXXXX-----XXXXXXXXXXXXXXXXXXXX
660 670 680 690 700
| | | | |
QDFDKSNPIVLRMTNDQIMCLERAFIDPLGLPDRPFYRHVIYAPSSHNKY
XX>>>*>-----XXXXXXXXXX->>*>----->***>
XX>>>*>-----XXXXXXXXXX->>*>----->***>
710 720 730 740 750
| | | | |
AGESFPGIYDALFDIESKVDPSKANGEVKRQIYVAAFTVQAAETLSEVA
----->-----XXXXXXXXXX----->XXXXXXXXXXXXXXXXXX
----->-----XXXXXXXXXX----->XXXXXXXXXXXXXXXXXX

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FIG. 15A



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FIG. 15B

* PREDICTION OF ANTIGENIC DETERMINANTS *

Done on sequence PMSANTIGEN.
Total number of residues is: 750.
Analysis done on the complete sequence.

The method used is that of Hopp and Woods.
The averaging group length is: 6 amino acids.

-> This is the value recommended by the authors <-

The three highest points of hydrophilicity are:

(1)	Ah=	1.62	:	From	63	to	68	:	Asp-Glu-Leu-Lys-Ala-Glu
(2)	Ah=	1.57	:	From	132	to	137	:	Asn-Glu-Asp-Gly-Asn-Glu
(3)	Ah=	1.55	:	From	482	to	487	:	Lys-Ser-Pro-Asp-Glu-Gly

Ah stands for: Average hydrophilicity.

Note that, on a group of control proteins, only the highest point was in 100% of the cases assigned to a known antigenic group. The second and third points gave a proportion of 33% of incorrect predictions.

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FIG. 16-1

The best scores are:

CHKTFER	G.gallus mRNA for transferrin receptor	initn	initl	opt
RATTRFR	Rat transferrin receptor mRNA, 3' end.	203	120	321
HUMTFRR	Human transferrin receptor mRNA, complete cd	164	164	311
		145	145	266

CHKTFER G.gallus mRNA for transferrin receptor 203 120 321
51.9% identity in 717 nt overlap

1020	1030	1040	1050	1060	1070
pmsgen	TGTCAGCGTGGAATAATCCTAAATCTGAATGGTGCAGGAGACCCCTCTCACACCAGGTTA				
CHKTFE	TACACTTATCCCATTCGGACATGCCACCTTGGAACCTGGAGACCCCTTACACCCAGGCTT				
990	1000	1010	1020	1030	1040

1080	1090	1100	1110	1120	1130
pmsgen	CCCAGCAATGAATATGCTTATAGCGGTGGAATTGCAGAGGCTGTGGTCTTCCAAGTAT				
CHKTFE	CCCTTCGTTCAACCACACCCCA---GTTCCACCAGTTGAATCTTCAGGACTACCCACAT				
1050	1060	1070	1080	1090	1100

1140	1150	1160	1170	1180	1190
pmsgen	TCCTGTTCATCCAATTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGCTC				
CHKTFE	TGCTGTTCAGACCATCTCTAGCAGTGCGACGACCCAGGCTGTTTCAGCAAAATGGATGGAGA				
1110	1120	1130	1140	1150	1160

FIG. 16-2

[illegible]

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FIG. 16-3

```
1440      1450      1460      1470      1480      1490
pmsgen AGCTGTTGTTCAATGAAATTGTGAG--GAGCTTTGGAACACTGAAAGGAGGAGGAG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CHKTFE TGCTATATTGTTGGAACCTTGCCCGTGTGATCTCAGACATAGTGAAAAACGAGGCTACAA
1390      1400      1410      1420      1430      1440

1500      1510      1520      1530      1540      1550
pmsgen ACCTAGAAAGAAATTTGTTTGCAGCTGGGATGCAGAGAAATTTGGTCTTCTGGTTC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CHKTFE ACCGAGCGAAGCATCATCTTTGCTAGCTGGAGTGCAGGAGACTACGGAGCTGTGGGTGC
1450      1460      1470      1480      1490      1500

1560      1570      1580      1590      1600      1610
pmsgen TACTGAGTGGGCAGAGAGAAATTCAGACTCCTTCAAGAGCGTGGCGTTATATTA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CHKTFE TACTGAATGGCTGGAGGGTACTCTGCCATGCTGCATGCCAAAGCTTTCACATTACATCA-
1510      1520      1530      1540      1550      1560

1620      1630      1640      1650      1660      1670
pmsgen TGC-TGACTCATCTATAGAAAGAACTA-CACTCTGAGAGTTGATGTACACCGCTGATG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CHKTFE -GCTTGGATGCTCCAGTCCCTGGGAGCAAGCCCATGTCAAGATTTCTGCCAGCCCCCTTGCTG
1570      1580      1590      1600      1610      1620
```

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FIG. 16-4

```
1680      1690      1700      1710      1720      1730
pmsgen  TACAGCTTGGTACACAACCTAACAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGC
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
CHKTFE  TATATGCTGCTGGGAGTATTATGAAGGGGTGAAGAATCCAGCAGCAGTCTCAGAGAGC
1630      1640      1650      1660      1670      1680

1740      1750      1760      1770      1780      1790
pmsgen  AAATCTCTTTATGAAGTTGGACTAAAAAAGTCCTTCCCCAGAGTTCAGTGGCATGCCCC
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
CHKTFE  -----CTCTATAACAGACTTGGCCCAGACTGGGTAAAGCAGTTGTTCCCTCTTGGCCCTGGA
1690      1700      1710      1720      1730
```

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FIG. 16-5

```

RATRRFR  Rat transferrin receptor mRNA, 3' end.      164  164  311
55.5% identity in 560 nt overlap

          1210  1220  1230  1240  1250
pmsgen  CCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAAATGTTGGACCTGGCTT-
          :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
RATTRF  TGCAGAAAAGCTATTCAAAAACATGGGAAGGAACTGTCCCTAGTTGGAATATAGATTC
        610  620  630  640  650  660

          1260  1270  1280  1290  1300  1310
pmsgen  -TACTGGAAACTTTTCTACACAAAAGTCAAGATGCACATC-CACTCT-ACCAATG----
          :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
RATTRF  CTCATGTAAAGCTGGAACTTTCACAGAAATCAAAATGTGAAGCTCACTGTGAACAATGTACT
        670  680  690  700  710  720

```

	1320	1330	1340	1350	1360	1370
pmsgen	--AAGTGACAAGAA	TTACAA	TGTGATAGG	TACTCTCAGAGG	CAGTGA	ACCAGACAG
	:::	:::	:::	:::	:::	:::
RATTRF	GAAAGAAAC	AAGAA	TACTTAA	CATCTTTGGCG	TTATTAAAGG	CTATGAGGA
730	740	750	760	770	780	

[illegible]

	1440	1450	1460	1470	1480
pmsgen	T-GGAGCAGCTGTTCATGAATTGTGAGGAGCTTTGGAAACA-CTGA--	-AAAAAGCAA			
	: : : : : : : : : : : : : : : : : :				
RATTRF	TGGGAACAGGTCTT-CTGTTGAAAACCTTGCCCCAAGTATTCTCAGATATGATTTCAAAAGAT				
	850	860	870	880	890
					900

	1490	1500	1510	1520	1530	1540
ppmsgen	GGTGGAGACCTAGAAACAATT	TTGTTGCAAGCTGGGATGCAGAA	TTTGGTCTT			
	::: X :::	::: :::	::: :::	::: :::	::: :::	::: :::
RATRF	GGATTAGACCCAGCAGGAGT	ATTATCTTTGCCAGCTGGACTGCAGGAG	ACTATGGAGCT			
	910	920	930	940	950	960

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FIG. 16-7

```
1550      1560      1570      1580      1590      1600
pmsgen  CTGGTTCTACTGAGTGGGCACAGGAGAA---TTCAAGACTCCTTCAAGAGCGTGCGGTG
      ::::: : ::::: : ::::: : X  ::::: : ::::: : ::::: :
RATRF   GTGGTCCGACTGAGTGGCTGGAGGGGTACCTTTCATCTTTGCATCTAAAG---GCTTTC
970      980      990      1000      1010      1020

1610      1620      1630      1640      1650      1660
pmsgen  GCTTATATTAATGCTGACTCATCTATAGAGGAACTA-CACTCTGAGAGTTGATTGTAC
      ::::: : ::::: : ::::: : ::::: : ::::: : ::::: :
RATRF   ACTTACATTAAAT-CTGGATAAAGTCGTCCTGGGTACTAGCAACTTCAAGGTTTCTGCCAG
1030      1040      1050      1060      1070      1080

1670      1680      1690      1700      1710      1720
pmsgen  ACCGCTGATGTACAGCTTGGTACACAACCTAACAAAGAGCTGAAAGC-CCTGATGAAG
      ::::: : ::::: : ::::: : ::::: : ::::: : ::::: :
RATRF   CCCCCATTATATACACTTATGGGGAAGATAATGCAGGA--CGTAAAGCATCCGA-----
1090      1100      1110      1120      1130
```

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FIG. 16-8

```

1730      1740      1750      1760      1770
pmsgen GCTTTGAAGGCAAAATCTCTTTAT-GAA-----AGTTGGACTAAATAAGTCCCTTCCCCCAG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RATTRF ---TTGATGGAAATATCTATATCGAAACAGTAATTGGATTAGCAAAATTGAGGAACTTT
1140      1150      1160      1170      1180      1190

1780      1790      1800      1810      1820      1830
pmsgen AGTCAGTGGCATGCCCCAGGATAAGCAAATTGGGATCTGGAAATGATTTGAGGTGTTCT

RATTRF CCTGGACAAATGCTGCATTCCCTTTCTTGCAATATTCAGGAATCCCAGCAGTTTCTTTCT
1200      1210      1220      1230      1240      1250
```

HUMTFR	Human transferrin receptor mRNA, complete cd	145	145	266
54.3%	identity in 464 nt overlap			

	1400	1410	1420	1430	1440	1450
pmsgen	CCGGACTCATGGGTGTTTGGTGATATGACCTCAGAGT-GGAGCACCTGTTGTTTCATG					
	: :	: : : : : :	: : : : : :	: : : : : :	: : : : : :	: :
HUMTFR	GAGAGATGCATGGGGCCCTGGAGCTGCAAAATC-CCGTGTAGGCACAGCTCTCCTATTGA					
1320	1330	1340	1350	1360	1370	

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FIG. 16-10

	1460	1470	1480	1490	1500
pmsgen	AAATG---	TCAGGAGCTTTGGAACACTGAA	AAAGGAGGTGGAGACCTAGA	GAACAA	
	:: :: ::	:: :: ::	:: :: ::	X :: ::	:: :: ::
HUMTFR	AACTGCCAGATGTTCTCAGATATG	GTCTTAAAGATGGGTTTCAGCC	AGCAGCA		
	1380	1390	1400	1410	1420
					1430
	1510	1520	1530	1540	1550
pmsgen	TTTGTTCGAAGCTGGGATGCAGA	GAATTTGGTCTTCTTGTTCTACT	GGCAG		
	:: :: ::	:: :: ::	:: :: ::	:: :: ::	:: :: ::
HUMTFR	TTATCTTTGCCAGTTGGAGTGCTG	GAGACTTTGGATCGGTTGGTGCC	ACTGAATGGCTAG		
	1440	1450	1460	1470	1480
					1490
	1570	1580	1590	1600	1610
pmsgen	A-GGAGAA	TTCAAGACTCCTTCAAGAGCG	TGCGCTTATATTAATGCT	CACTCT	
	:: :: ::	:: :: ::	:: :: ::	:: :: ::	X :: ::
HUMTFR	AGGATACCTTTCGTC-CCTGC	ATTAAAGGCTTTCACCTTATATTA	CTCTGGATAA	AGCG	
	1500	1510	1520	1530	1540
					1550
	1630	1640	1650	1660	1670
pmsgen	ATAGAAG	AACTACACTCTGAGAGTTGAT	TGTACACCGCTGATGTACA	-GCTTGGT-AC	
	:: :: ::	:: :: ::	:: :: ::	:: :: ::	:: :: ::
HUMTFR	GTTCTTGGTACCAGCAACTTCA	AGGTTTCTGCCAGCCCACTGTTGTATAC	CGCTTATTGAG		
	1560	1570	1580	1590	1600
					1610

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FIG. 16-11

1690	1700	1710	1720	1730	1740
pmgen	ACAAACCTAACAAAGAGCTGAAAGCCCTGATGAAGGCTTTGAAGGCAAAATCTCTTTATG				
	: : : :	: : : :			
HUMTFR	AAAACAATGC AAAATGTGAAGCATCCGGTACTGGGCAATTCTATATCAGGACAGCAAC				
1620	1630	1640	1650	1660	1670

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FIGURE 17A

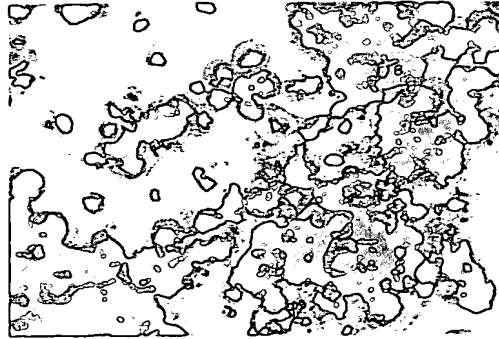
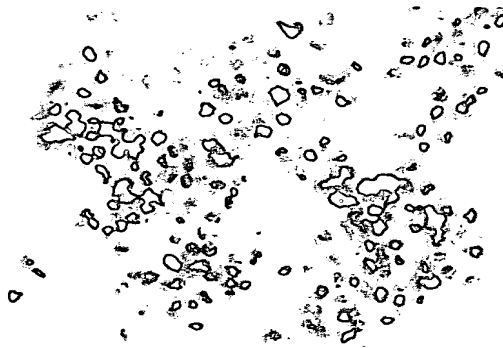


FIGURE 17B

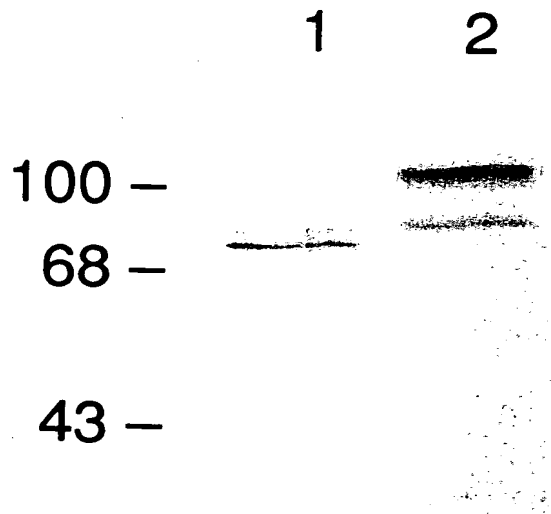


FIGURE 17C



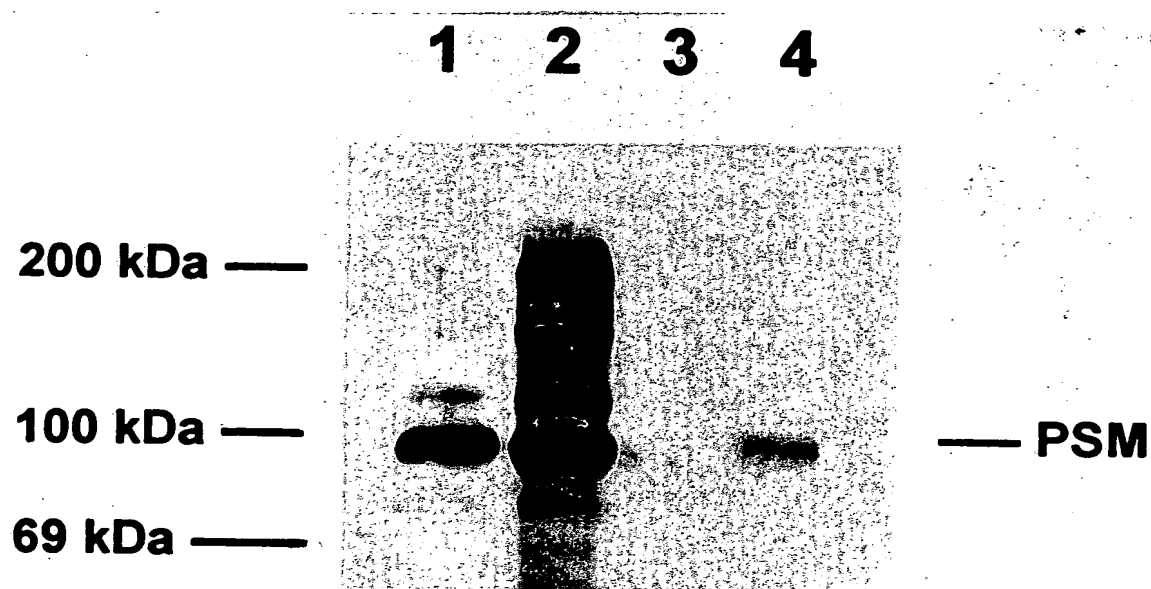
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FIGURE 18



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FIGURE 19



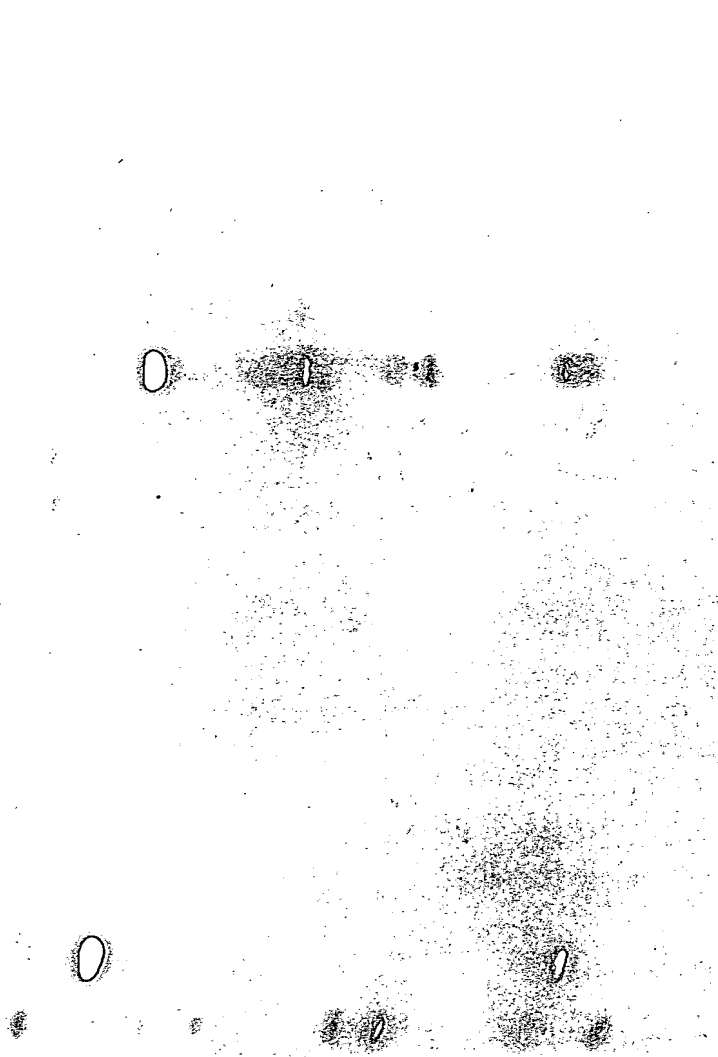
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FIGURE 20

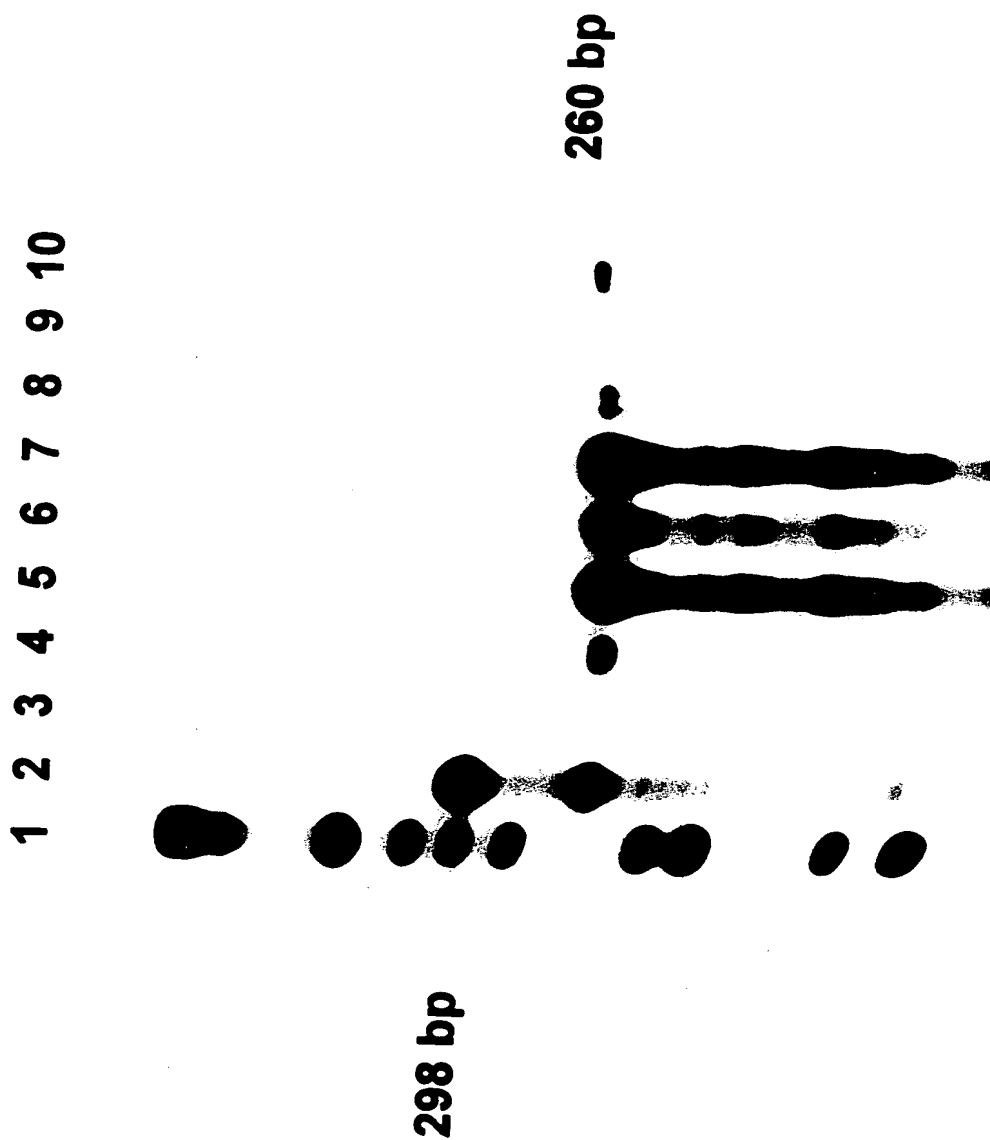
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15

400



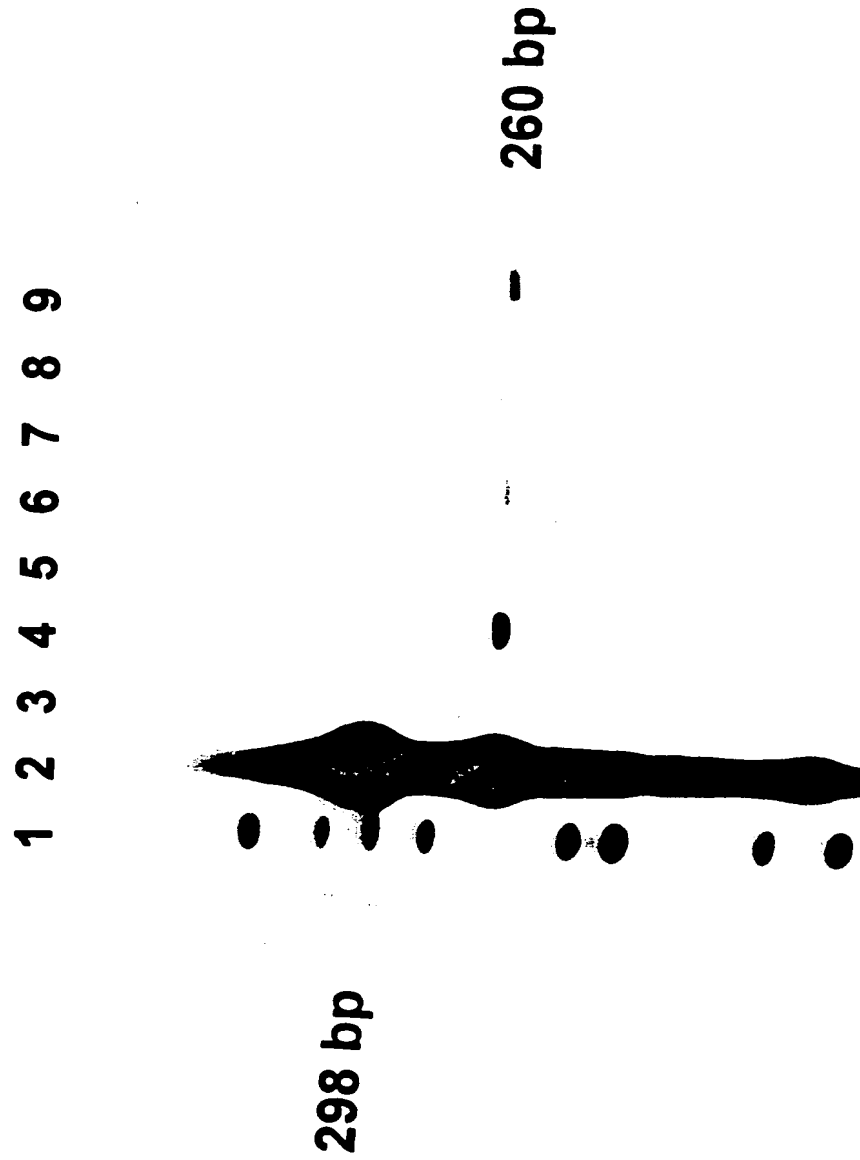
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FIGURE 21



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FIGURE 22



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FIGURE 23

CELL LINE/TYPE	11p11.2-13 REGION	METASTATIC	PSM RNA DETECTED	PSM DNA DETECTED
LNCap			++	ND
HUMAN PROSTATE			++	ND
A9 (FIBROSARCOMA)	NO	NO	-	-
A9(11) (A9+HUM. 11)	YES	NO	-	REPEAT
AT6.1 (RAT PROSTATE)	NO	YES	-	-
AT6.1-11-c11	YES	NO	+	++
AT6.1-11-c12	NO	YES	-	-
R1564 (RAT MAMMARY)	NO	YES	-	-
R1564-11-c14	YES	YES	-	+
R1564-11-c15	YES	YES	-	REPEAT
R1564-11-c16	YES	YES	-	ND
R1564-11-c12	YES	YES	ND	+

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FIGURE 24A

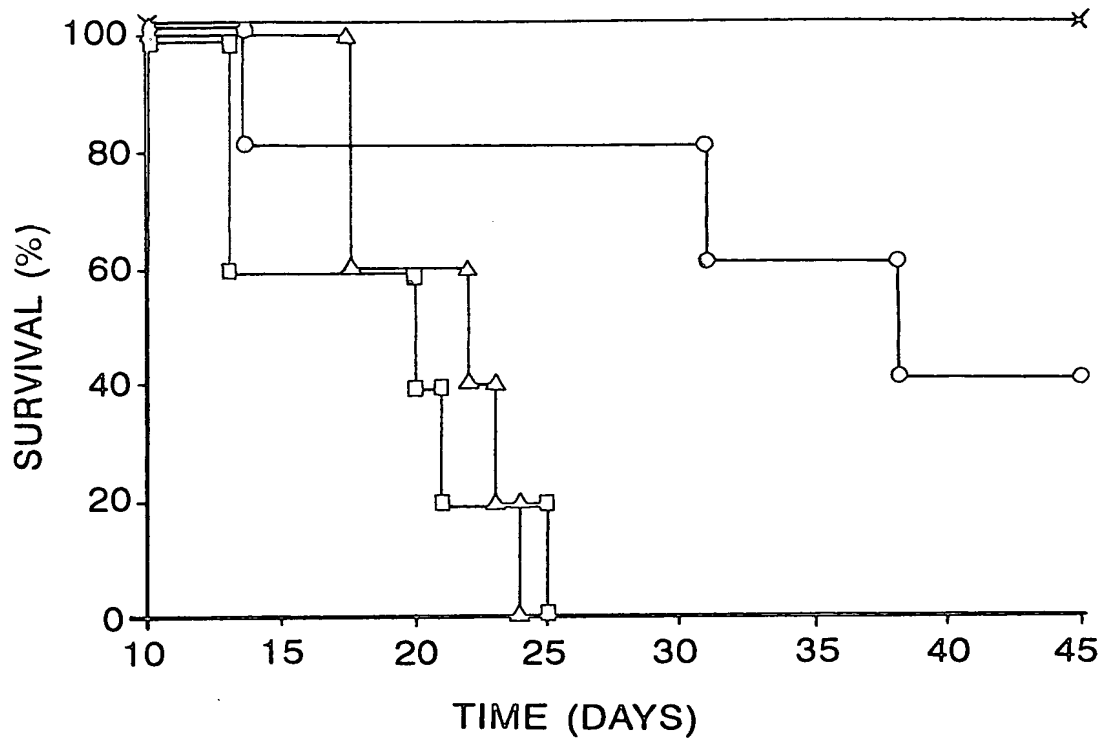
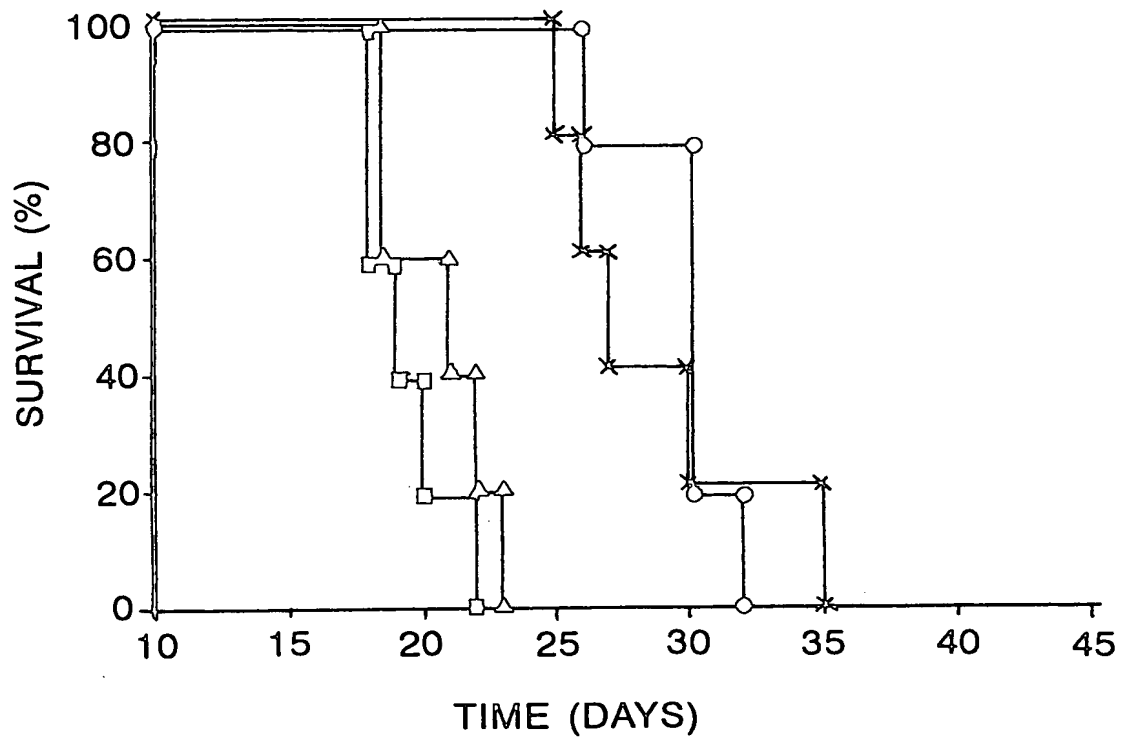


FIGURE 24B



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FIGURE 25A

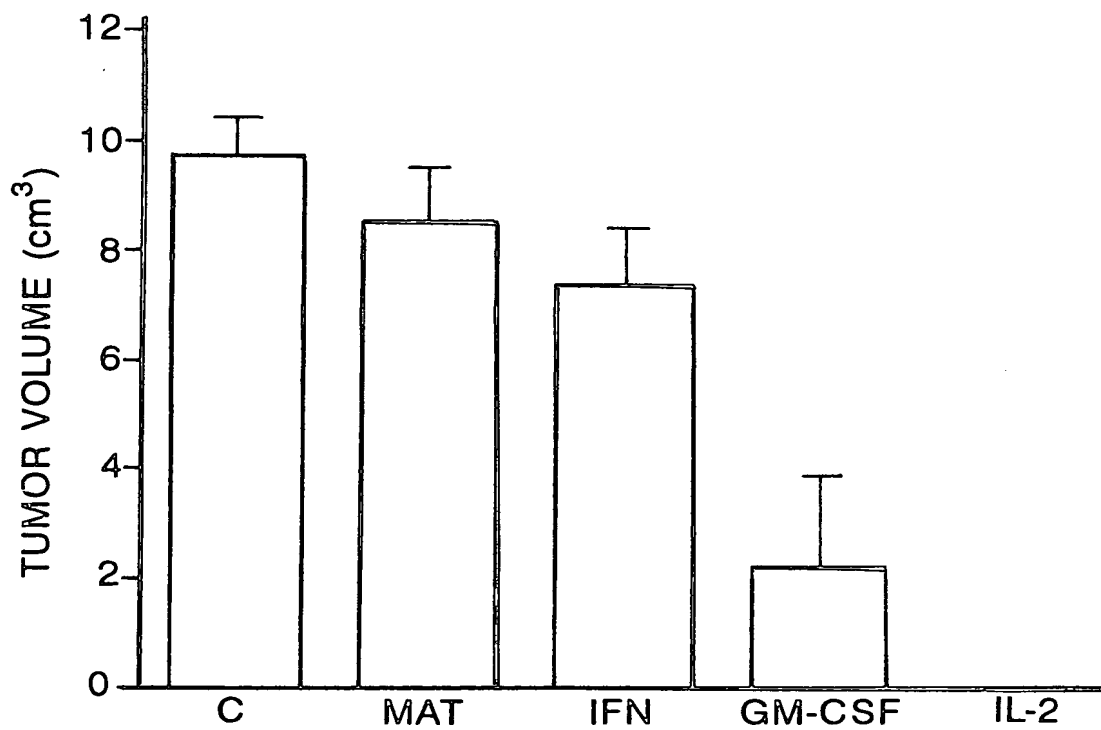
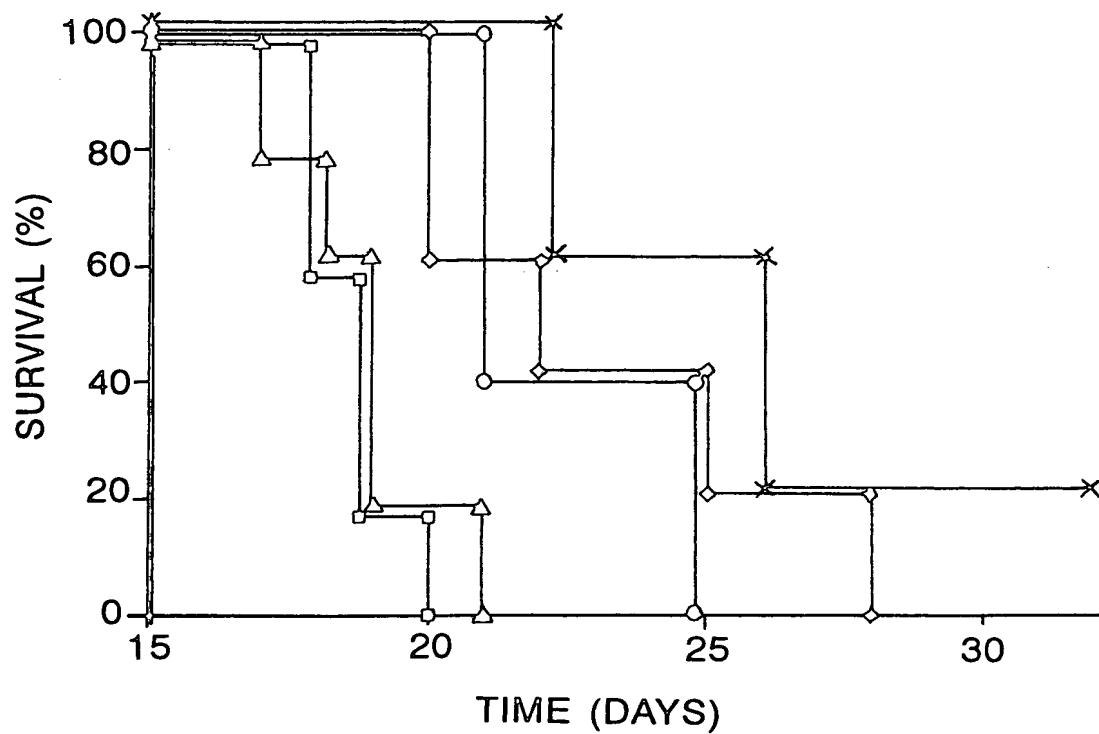
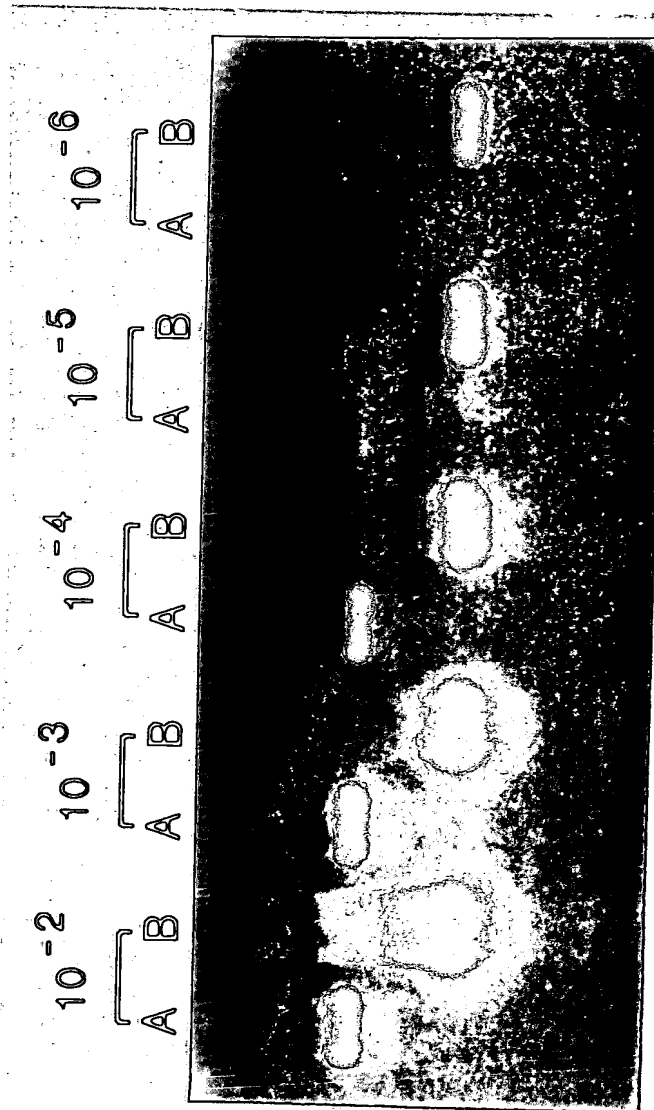


FIGURE 25B



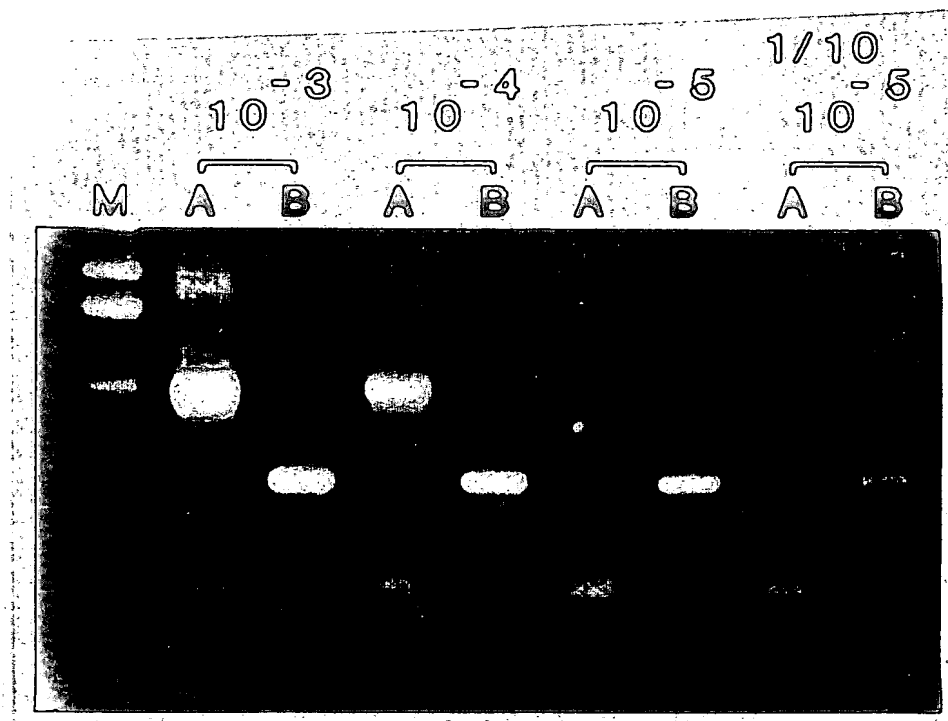
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FIGURE 26



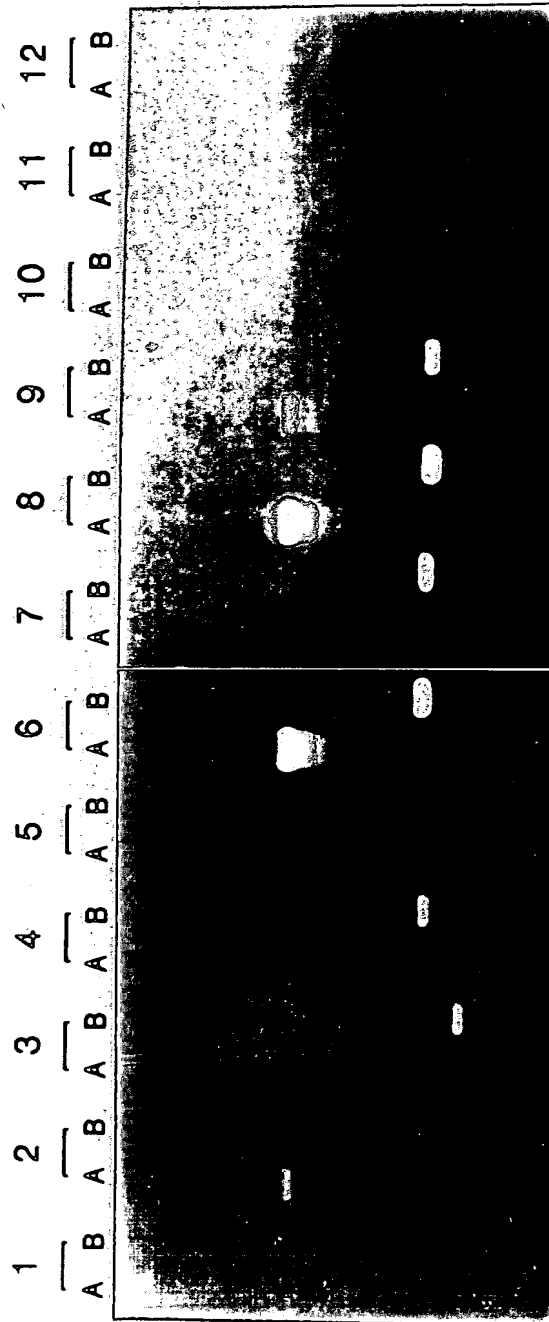
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FIGURE 27



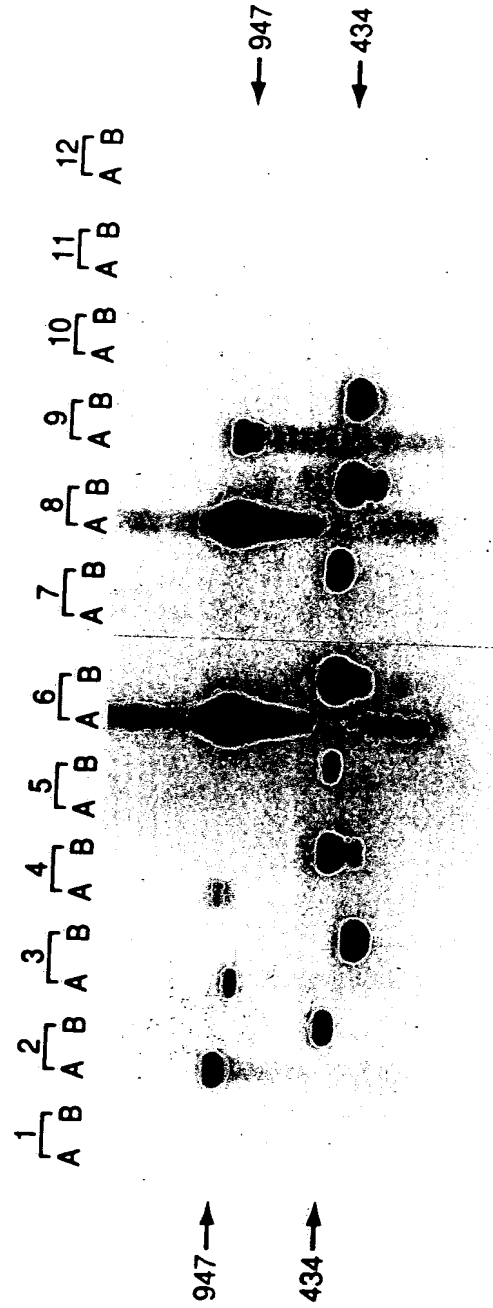
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FIGURE 28



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FIGURE 29



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FIGURE 30

Patient	Stage	Treatment	PSA	PAP	PSA-PCR	PSM-PCR
1	T2NxMo	None	8.9	0.7	—	+
2	T2NoMo	RRP 7/93	6.1	—	—	+
3	T2CNoMo	PLND 5/93	4.5	0.1	—	+
4	T2BNoMo	RRP 3/92	NMA	0.4	—	+
5	T3NxMo	Proscar + Flutamide	51.3	1.0	—	+
6	Recur T3	I-125 1986	54.7	1.4	—	+
7	T3ANoMo	RRP 10/92	NMA	0.3	—	+
8	T3NxMo	XRT 1987	7.5	0.1	—	—
9	T3NxMo	Proscar + Flutamide	35.4	0.7	—	—
10	D2	S/P XRT Flutamide + Emcyt	311	4.5	+	+
11	D2	RRP 4/91 Lupron 10/92 Velban + Emcyt 12/92	1534	1.4	+	+
12	T2NoMo	RRP 8/91	NMA	0.5	—	+
13	T3NoMo	RRP 1/88 Lupron + Flutamide 5/92	0.1	0.3	—	—
14	D1	PLND 1989 XRT 1989	1.6	0.4	—	—
15	D1	Proscar + Flutamide	20.8	0.5	—	—
16	T2CNoMo	RRP 4/92	0.1	0.3	—	—

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